AMENDMENTS TO THE CLAIMS

Please amend the claims as set forth below. The complete set of claims is provided below in compliance with the Revised 37 C.F.R. § 1.121, Effective July 30, 2003. The status of each claim is shown next to each claim number; current additions are shown by underlines and deletions are shown by strikethrough.

1. (Currently Amended) A set of promoter sequences which is suitable for optimizing the expression of a gene in a selected microorganism **selected from the group consisting of lactic acid bacteria, *Bacillus, E. coli, Pseudomonas* and yeast**, said set of promoter sequences covering a range of promoter activities for said gene in said selected microorganism in small steps each step changing the activity by 50-100%, each promoter sequence of said set of promoter sequences comprising a double stranded DNA sequence, the sense strands of which comprise

at least two consensus sequences, said at least two consensus sequences corresponding to conserved sequences identified in said selected microorganism, at least half of each of said consensus sequences being kept constant in the set of promoter sequences, the at least two consensus sequences, when the selected microorganism is

a) a bacterium, **wherein at least one of** said at least two consensus sequences **is TATAAT and at least one of said at least two consensus sequences is** ~~being~~ selected from the group consisting of ~~TATAAT,~~ TTGACA and an activator binding site upstream of the TATAAT sequence, or

b) is a yeast, wherein at least one of said at least two consensus sequences ~~being selected from the group consisting of~~ a TATA-box and at least one of said at least two consensus sequences is a UAS upstream of said TATA-box and,

between said consensus sequences or flanking at least one of said consensus sequences, at least one nucleotide spacer sequence, at least part of which, relative to the corresponding spacer sequence of the identified promoter, is varied by random incorporation of nucleotides that are selected ~~Rom~~ from the group consisting of the nucleobases A, T, C and G.

2. (Previously Presented) A set of promoter sequences according to claim 1 wherein at least 10 nucleotides in the at least one nucleotide spacer sequence are selected randomly from the group consisting of the nucleobases A, T, C and G.

3. (Currently Amended) A set of promoter sequences according to claim 1 wherein each of the promoter sequences comprises a regulatory DNA sequence ~~imparting a specific regulatory feature to each of the promoter sequences~~.

4. (Currently Amended) A set of promoter sequences according to claim 1 wherein each of the promoter sequences ~~members~~ comprises at least one recognition site for a restriction endonuclease.

5. (Cancelled)

6. (Previously Presented) A set of promoter sequences according to claim 1 wherein the selected microorganism is a bacterium where the consensus sequences comprise at least 3 conserved nucleotides of the -10 signal TATAAT.

7. (Previously Presented) A set of promoter sequences according to claim 1 wherein the selected microorganism is a bacterium where the consensus sequences comprise at least 3 conserved nucleotides of the -35 signal TTGACA.

8. (Previously Presented) A set of promoter sequences according to claim 1 wherein the selected miroorganism is a bacterium where each of the promoter sequences comprise at least one conserved motif selected from the group consisting of AGTT at positions -44 to -41, TATTC at positions -40 to -35, TG at position -15 to -14 and GTACTGTT at positions +1 to +8.

9. (Previously Presented) A set of promoter sequences according to claim 1 comprising at least two promoter sequences selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42.

10. (Previously Presented) A set of promoter sequences according to claim 7 wherein the spacer sequence between the -35 and the -10 signal is 14-23 bp.

11. (Previously Presented) A set of promoter sequences according to claim 5 wherein the promoter sequences comprise a sequence selected from the group consisting of SEQ ID NO: 1 and SEQ ID NO:2.

12. (Cancelled)

13. (Previously Presented) A set of promoter sequences according to claim 1 wherein the selected microorganism is a yeast where the consensus sequences comprise a TATA box and at least one upstream activation sequence (UAS).

14. (Currently Amended) A set of promoter sequences according to claim 1 ~~wherein the~~ comprising a promoter sequence derived from ~~is~~ SEQ ID NO:3.

15. (Previously Presented) An isolated set of promoter sequences according to claim 1 comprising at least two promoter sequences selected from the group consisting of SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:58.

16. (Currently Amended) A method of constructing a set of promoter sequences which is suitable for optimizing the expression of a gene in a selected microorganism, said set of promoter sequences covering a range of promoter activities for said gene, the method comprising:

(i) identifying in said microorganism a promoter sequence comprising at least two consensus sequences, which consensus sequences correspond to conserved sequences identified in said microorganism, at least one of the consensus sequences being flanked by a non-conserved nucleotide spacer sequence or both of said consensus sequences being separated by the non-conserved nucleotide spacer sequence, the at least two consensus sequences, when the selected microorganism is

(a) a prokaryotic microorganism, wherein at least one of said at least two consensus sequences is TATAAT and at least one of said at least two consensus sequences is ~~being~~ selected from the group consisting

of ~~TATAAT,~~ TTGACA and an activator binding site upstream of the TATAAT sequence, or

(b) an eukayotic microorganism, **wherein at least one of** said at least two consensus sequences ~~being selected from the group consisting of~~ a TATA-box and **at least one of said at least two consensus sequences is** a UAS upstream of said TATA-box,

(ii) constructing a set of single stranded DNA sequences each of which comprises at least half of each of the consensus sequences, and a non-conserved nucleotide spacer sequence, at least part of which is varied by a random incorporation of nucleotides selected from the group consisting of the nucleobases A, T, C and G, whilst keeping the at least half of the consensus sequences constant, and

(iii) converting the single stranded DNA sequences into double stranded DNA sequences to obtain the set of promoter sequences covering a range of promoter activities for said gene.

17. (Currently Amended) A method according to claim 16 wherein a plurality of promoter sequences is selected from the set of promoter sequences, said plurality of promoter sequences covering, in said selected **microorganisms** ~~mircoorganisms~~, a range of promoter activities for said gene, in steps, each step changing the promoter activity by 50-100%.

18. (Currently Amended) A method of controlling in a microorganism the expression of at least one gene product, said method comprising at least one step of changing the expression level of the at least one gene comprising

(i) selecting from a set of promoter sequences **a subset of said promoter sequences** suitable for optimizing the expression of the at least one gene in a

selected microorganism, said **subset of the** set of promoter sequences covering a range of promoter activities for said gene is said selected microorganism in
small steps each step changing the activity by 50-100%, each promoter sequence of said set of promoter sequences comprising a double stranded DNA sequence, the sense strands of which comprise

at least two consensus sequences, said at least two consensus sequences corresponding to conserved sequences identified in said microorganism, at least half of each of said consensus sequences being kept constant in the set of promoter sequences, the at least two consensus sequences, when the selected microorganism is

a) a prokaryotic microorganism, **wherein at least one of** said at least two consensus sequences **is TATAAT and at least one of said at least two consensus sequences is** ~~being~~ selected from the group consisting of ~~TATAAT,~~ TTGACA and an activator binding site upstream of the TATAAT sequence, or

b) an eukaryotic microorginism, **wherein at least one of** said at least two consensus sequences **is TATAAT and at least one of said at least two consensus sequences is** ~~being~~ selected from the group consisting of ~~TATAAT,~~ TTGACA and an activator binding site upstream of the TATAAT sequence and,

between said consensus sequences or flanking at least one of said consensus sequences, at least one nucleotide spacer sequence, at least part of which, relative to the corresponding spacer sequence of the identified promoter, is

varied by random incorporation of nucleotides that are selected from the group consisting of the nulcleobases A, T, C and G,

(ii) transforming said **subset of** ~~set of~~ promoter sequences into cells of the organism, placing in each of said cells the gene to be expressed under the control of at least one promoter of the set,

(iii) cultivating the transformed cells to obtain clones thereof and selecting among said clones a clone having, relative to an otherwise identical clone where the at least one gene is under the control of its native promoter, a higher or a lower expression of the at least one gene product.

19. (Cancelled)

20. (Cancelled)

21. (Currently Amended) A method of isolating a promoter sequence being capable of optimizing the expression of at least one gene in a pathway **of the cellular metabolism** or a gene expressing a desired gene product in a selected microorganism, the method comprising

(i) constructing, using the method of claim 16, a set of promoters covering a range of promoter activities for said gene, in steps, each step changing the promoter activity by 50-100%,

(ii) transforming said set of promoters into cells of the selected microorganism, placing in each of said cells the gene to be expressed under the control of at least one promoter of the set,

(iii) cultivating the transformed cells to obtain clones thereof and selecting among said clones a clone having, relative to an otherwise identical clone where the at least one gene in the pathway or the gene expressing the

desired gene product is under the control of its native promoter, a higher or a lower flux of ~~the~~ a cellular metabolite or a higher or a lower expression of the desired gene product, and

(iv) isolating said promoter sequence from the clone **selected in step**.

22. (Previously Presented) An isolated promoter sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:58.

23. (Previously Presented) A set of promoters according to claim 1 suitable for optimizing the expression of a gene in a bacterium wherein the promoter sequences comprise a sequence selected from the group consisting of AGTT, TATTC, TG, TTGA, TTGG, and GTACTGTT.

24. (Cancelled)

25. (Previously Presented) A set of promoters according to claim 1 where, when the selected microorganism is a yeast, the TATA-box is the TATAAA sequence.

26. (Cancelled)

27. (Previously Presented) A set of promoters according to claim 1 where, when the selected microorganism is a yeast, the UAS is UAS_{GCN4p}.